OS90
1128

#2

OIPE

RAW SEQUENCE LISTING   DATE: 01/02/2002
PATENT APPLICATION: US/09/912,717   TIME: 14:52:54

Input Set : N:\Crf3\RULE60\09912717.raw
Output Set: N:\CRF3\01022002\I912717.raw

SEQUENCE LISTING
```
 3 (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Hillman, Jennifer L.
 6                      Corley, Neil C.
 7                      Baughn, Mariah R.
 9      (ii) TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE
10                              HOMOLOG
12     (iii) NUMBER OF SEQUENCES: 3
14      (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16           (B) STREET: 3174 Porter Drive
17           (C) CITY: Palo Alto
18           (D) STATE: CA
19           (E) COUNTRY: USA
20           (F) ZIP: 94304
22       (v) COMPUTER READABLE FORM:
23           (A) MEDIUM TYPE: Diskette
24           (B) COMPUTER: IBM Compatible
25           (C) OPERATING SYSTEM: Windows
26           (D) SOFTWARE: FastSEQ for Windows Version 2.0b
28      (vi) CURRENT APPLICATION DATA:
C--> 29      (A) APPLICATION NUMBER: US/09/912,717
C--> 30      (B) FILING DATE: 24-Jul-2001
31           (C) CLASSIFICATION:
33     (vii) PRIOR APPLICATION DATA:
34           (A) APPLICATION NUMBER: 09/565,910
35           (B) FILING DATE:
39    (viii) ATTORNEY/AGENT INFORMATION:
40           (A) NAME: Cerrone, Michael C
41           (B) REGISTRATION NUMBER: 39,132
42           (C) REFERENCE/DOCKET NUMBER: PF-0532 US
44      (ix) TELECOMMUNICATION INFORMATION:
45           (A) TELEPHONE: 650-855-0555
46           (B) TELEFAX: 650-855-0572
47           (C) TELEX:
50 (2) INFORMATION FOR SEQ ID NO: 1:
52       (i) SEQUENCE CHARACTERISTICS:
53           (A) LENGTH: 314 amino acids
54           (B) TYPE: amino acid
55           (C) STRANDEDNESS: single
56           (D) TOPOLOGY: linear
58     (vii) IMMEDIATE SOURCE:
59           (A) LIBRARY: PROSNON01
60           (B) CLONE: 2278458
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 Met Ser Val Gly Phe Ile Gly Ala Gly Gln Leu Ala Tyr Arg Phe Thr
65  1               5                  10                  15
```

ENTERED

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```
 66  Ala Ala Gly Ile Leu Ser Ala His Lys Ile Ile Ala Ser Ser Pro Glu
 67              20                  25              30
 68  Met Asn Leu Pro Thr Val Ser Ala Leu Arg Lys Met Gly Val Asn Leu
 69          35              40                  45
 70  Thr Arg Ser Asn Lys Glu Thr Val Lys His Ser Asp Val Leu Phe Leu
 71      50                  55                  60
 72  Ala Val Lys Pro His Ile Ile Pro Phe Ile Leu Asp Glu Ile Gly Ala
 73  65                  70                  75                  80
 74  Asp Val Gln Ala Arg His Ile Val Val Ser Cys Ala Ala Gly Val Thr
 75                  85                  90                  95
 76  Ile Ser Ser Val Glu Lys Lys Leu Met Ala Phe Gln Pro Ala Pro Lys
 77              100                 105                 110
 78  Val Ile Arg Cys Met Thr Asn Thr Pro Val Val Val Gln Glu Gly Ala
 79              115                 120                 125
 80  Thr Val Tyr Ala Thr Gly Thr His Ala Leu Val Glu Asp Gly Gln Leu
 81      130                 135                 140
 82  Leu Glu Gln Leu Met Ser Ser Val Gly Phe Cys Thr Glu Val Glu Glu
 83  145                 150                 155                 160
 84  Asp Leu Ile Asp Ala Val Thr Gly Leu Ser Gly Ser Gly Pro Ala Tyr
 85                  165                 170                 175
 86  Ala Phe Met Ala Leu Asp Ala Asp Gly Gly Val Lys Met Gly Leu Pro
 87              180                 185                 190
 88  Arg Arg Leu Ala Ile Gln Leu Gly Ala Gln Ala Leu Leu Gly Ala Ala
 89          195                 200                 205
 90  Lys Met Leu Leu Asp Ser Glu Gln His Pro Cys Gln Leu Lys Asp Asn
 91      210                 215                 220
 92  Val Cys Ser Pro Gly Gly Ala Thr Ile His Ala Leu His Phe Leu Glu
 93  225                 230                 235                 240
 94  Ser Gly Gly Phe Arg Ser Leu Leu Ile Asn Ala Val Glu Ala Ser Cys
 95                  245                 250                 255
 96  Ile Arg Thr Arg Glu Leu Gln Ser Met Ala Asp Gln Glu Lys Ile Ser
 97              260                 265                 270
 98  Pro Ala Ala Leu Lys Lys Thr Leu Leu Asp Arg Val Lys Leu Glu Ser
 99          275                 280                 285
100   Pro Thr Val Ser Thr Leu Thr Pro Ser Ser Pro Gly Lys Leu Leu Thr
101        290                 295                 300
102   Arg Ser Leu Ala Leu Gly Gly Lys Lys Asp
103   305                 310
105  (2) INFORMATION FOR SEQ ID NO: 2:
107      (i) SEQUENCE CHARACTERISTICS:
108          (A) LENGTH: 1742 base pairs
109          (B) TYPE: nucleic acid
110          (C) STRANDEDNESS: single
111          (D) TOPOLOGY: linear
113     (vii) IMMEDIATE SOURCE:
114          (A) LIBRARY: PROSNON01
115          (B) CLONE: 2278458
117      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
119   GCGCCATCAG CCGCCCGGGA GATATCCGCC GGGGGAGAAT AGGGTTGCAC CATCCCAGAA        60
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```
120   GCTGCTGTTA GCTCGCCGGT CCTCGGCACG CCGCCCGTTC GCCCCTGCGC TGTCCGCCCT   120
121   TCCCCTAGCG TTACTTCCGG TCCCTCGCTG AGGGGGTTCG TGCGGCTCCC AGGAGGCGTG   180
122   AACCGCGGAC CATGAGCGTG GGCTTCATCG GGGCCGGCCA GCTGGCCTAT GCTCTGGCGC   240
123   GGGGCTTCAC GGCCGCAGGC ATCCTGTCGG CTCACAAGAT AATAGCCAGC TCCCCAGAAA   300
124   TGAACCTGCC CACGGTGTCC GCGCTCAGGA AGATGGGTGT GAACCTGACA CGCAGCAACA   360
125   AGGAGACGGT GAAGCACAGC GACGTCCTGT TTCTGGCTGT GAAGCCACAT ATCATCCCCT   420
126   TCATCCTGGA TGAGATTGGG GCCGACGTGC AAGCCAGACA CATCGTGGTC TCCTGTGCGG   480
127   CTGGTGTCAC CATCAGCTCT GTGGAGAAGA AGCTGATGGC ATTCCAGCCA GCCCCCAAAG   540
128   TGATTCGCTG CATGACCAAC ACACCTGTGG TAGTGCAGGA AGGCGCTACA GTGTACGCCA   600
129   CGGGCACCCA TGCCCTGGTG GAGGATGGGC AGCTCCTGGA GCAGCTCATG AGCAGCGTGG   660
130   GCTTCTGCAC TGAGGTGGAA GAGGACCTCA TCGATGCCGT CACGGGGCTC AGTGGCAGCG   720
131   GGCCTGCCTA TGCATTCATG GCTCTGGACG CATTGGCTGA TGGTGGGGTG AAGATGGGTT   780
132   TGCCACGGCG CCTGGCAATC CAACTCGGGG CCCAGGCTTT GCTGGGAGCT GCCAAGATGC   840
133   TGCTGGACTC GGAGCAGCAT CCATGCCAGC TTAAGGACAA TGTCTGCTCC CCTGGGGGAG   900
134   CCACCATCCA CGCCCTGCAC TTTCTAGAGA GTGGGGGCTT CCGCTCTCTG CTCATCAATG   960
135   CAGTTGAGGC CTCCTGTATC CGAACACGAG AGCTACAGTC CATGGCCGAC CAAGAAAAGA   1020
136   TCTCCCCAGC TGCCCTTAAG AAGACCCTCT TAGACAGAGT GAAGCTGGAA TCCCCCACAG   1080
137   TCTCCACACT GACCCCCTCC AGCCCAGGGA AGCTCCTCAC AAGAAGCCTG GCCCTGGGAG   1140
138   GCAAGAAGGA CTAAGGCAGC ATCTGTCCCC TCTGTGATTC AGAGCCCTTA GTTGAGAGCC   1200
139   CCTGCCGCCC CTGCCACCCC CCTGCCCCGC TCCCACCATT GCCCCTCCTC AGCTGTGCAA   1260
140   GGAGAAAGCA TGCTTAGGAA GTTTTCAGGT CCTTGTGATA AAACCTCCTT AAATCTGTTC   1320
141   AGACCAAGCA ATGCGAGCTT CCTCTCCTGT CCCATGTTGG AAGTTGCTCT GAAGGGGTGG   1380
142   TAGATGCTGG AAGCCAGACA CAACCCTGCG TACGCTGCTC AGTTGGTGGA GACTGGGGCT   1440
143   GGGACTGGAG TCAGCCCAGC TGGGAGGAGG GGCTGGGGAG GATCTGCAGC TGAAGCCCGA   1500
144   GGCAGGGTTG GTGTGATGCC AAGGCAAAGT GGTGAGGAGA AAACAGGAAA CGGGCTTTCT   1560
145   CTGAATTGGT AAATGGGAAA GAAGTGAGCA ACTTAAGATT GTCACAATTA ATCACAAGTG   1620
146   TACAGGATTA GACTGGGTTT ATATTTAACT CTTGCTTCAT AGGTGTACCA TTTAAAGAGT   1680
147   GTTATTTAAT GCTAAGTTTA ACTGCTTTAA TAAAGTTTAT TTTTAAATAT CAAAAAAAAA   1740
148   AA                                                                 1742
150 (2) INFORMATION FOR SEQ ID NO: 3:
152     (i) SEQUENCE CHARACTERISTICS:
153         (A) LENGTH: 315 amino acids
154         (B) TYPE: amino acid
155         (C) STRANDEDNESS: single
156         (D) TOPOLOGY: linear
158   (vii) IMMEDIATE SOURCE:
159         (A) LIBRARY: GENBANK
160         (B) CLONE: 189498
162    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
164   Met Ser Val Gly Phe Ile Gly Ala Gly Gln Leu Ala Phe Ala Lys Gly
165    1               5                  10                  15
166   Phe Thr Ala Ala Gly Val Leu Ala Ala His Lys Ile Met Ala Ser Ser
167           20                  25                  30
168   Pro Asp Met Asp Leu Ala Thr Val Ser Ala Leu Arg Lys Met Gly Val
169           35                  40                  45
170   Lys Leu Thr Pro His Asn Lys Glu Thr Val Gln His Ser Asp Val Leu
171      50                  55                  60
172   Phe Leu Ala Val Lys Pro His Ile Ile Pro Phe Ile Leu Asp Glu Ile
173   65                  70                  75                  80
```

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Output Set: N:\CRF3\01022002\I912717.raw

```
174   Gly Ala Asp Ile Glu Asp Arg His Ile Val Val Ser Cys Ala Ala Gly
175                   85              90              95
176   Val Thr Ile Ser Ser Ile Glu Lys Lys Leu Ser Ala Phe Arg Pro Ala
177                  100             105             110
178   Pro Arg Val Ile Arg Cys Met Thr Asn Thr Pro Val Val Val Arg Glu
179           115             120             125
180   Gly Ala Thr Val Tyr Ala Thr Gly Thr His Ala Gln Val Glu Asp Gly
181       130             135             140
182   Arg Leu Met Glu Gln Leu Leu Ser Thr Val Gly Phe Cys Thr Glu Val
183   145             150             155             160
184   Glu Glu Asp Leu Ile Asp Ala Val Thr Gly Leu Ser Gly Ser Gly Pro
185               165             170             175
186   Ala Tyr Ala Phe Thr Ala Leu Asp Ala Asp Gly Gly Val Lys Met Gly
187           180             185             190
188   Leu Pro Arg Arg Leu Ala Val Arg Leu Gly Ala Gln Ala Leu Leu Gly
189           195             200             205
190   Ala Ala Lys Met Leu Leu His Ser Glu Gln His Pro Gly Gln Leu Lys
191       210             215             220
192   Asp Asn Val Ser Ser Pro Gly Gly Ala Thr Ile His Ala Leu His Val
193   225             230             235             240
194   Leu Glu Ser Gly Gly Phe Arg Ser Leu Leu Ile Asn Ala Val Glu Ala
195               245             250             255
196   Ser Cys Ile Arg Thr Arg Glu Leu Gln Ser Met Ala Asp Gln Glu Gln
197           260             265             270
198   Val Ser Pro Ala Ala Ile Lys Lys Thr Ile Leu Asp Lys Val Lys Leu
199           275             280             285
200   Asp Ser Pro Ala Gly Thr Ala Leu Ser Pro Ser Gly His Thr Lys Leu
201       290             295             300
202   Leu Pro Arg Ser Leu Ala Pro Ala Gly Lys Asp
203   305             310             315
```

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PATENT APPLICATION: US/09/912,717   TIME: 14:52:55

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Output Set: N:\CRF3\01022002\I912717.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]